

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/451,739G

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
  
- 4      Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
  
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                                   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   This sequence is intentionally skipped  
  
                                   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
                                   <210> sequence id number  
                                   <400> sequence id number  
                                   000
  
- 9 X      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                                   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                                   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
  
- 11      Use of <220>     Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
                                   Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                   (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa     "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



<110> Jager, Dirk  
Scanlan, Matthew  
Gure, Ali  
Jager, Elke  
Knuth, Alexander  
Old, Lloyd  
Chen, Yao-tseng

<120> Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens,  
the Antigens per se, and Uses Thereof

<130> LUD 5615

<140> 09/451,739

<141> 1999-11-30

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Asn Val Ser Leu Met Arg Glu Ile Asp Ala Lys Tyr Gln Glu Ile Leu  
 35 40 45

Lys Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly  
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Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg  
 65 70 75 80

Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val  
 85 90 95

Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu  
 100 105 110

Phe Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys  
 115 120 125

Val Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys  
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Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu  
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 180 185 190

Lys Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn  
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Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile  
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Gly Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys  
 225 230 235 240

Val Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys  
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Arg Thr Arg Gln Val Asp Ser His Val Glu Leu Phe Glu Ala Gln Gln  
35 40 45

Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys Val Gly Ala Asp Arg  
50 55 60

Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys Pro Asn Ser Lys Arg  
65 70 75 80

Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu Asn Ala Ser Ser Asn  
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His Asp His Asp Asp Gly Ala Ser Gly Thr Pro Lys Glu Lys Lys Ala  
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Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala Lys Ala Glu Arg Glu  
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Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn Glu Pro Thr Tyr Cys  
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Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys Val Gly Leu Asn His  
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 85 90 95  
 Gln Ser Asp Lys Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn  
 100 105 110  
 Glu Asn Arg Glu Asn Ala Ser Ser Asn His Asp His Asp Asp Gly Ala  
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 Arg Ser Lys Ala Lys Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro  
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 Gly Glu Met Ile Gly Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe  
 180 185 190  
 His Phe Ser Cys Val Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr  
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 35 40 45

Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln  
 50 55 60

Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr  
 65 70 75 80

Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu  
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Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly  
 100 105 110

Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala  
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Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys  
 130 135 140

Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn  
 145 150 155 160

Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met  
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Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp  
 180 185 190

Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro  
 195 200 205

Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu  
 210 215 220

Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu  
 225 230 235 240

Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys  
 245 250 255

Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser

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Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu		
290	295	300
Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu		
305	310	315
Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln		
325	330	335
Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu		
340	345	350
Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu		
355	360	365
Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu		
370	375	380
Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr		
385	390	395
Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met		
405	410	415
Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr		
420	425	430
Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser		
435	440	445
Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu		
450	455	460
Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile		
465	470	475
Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp		
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 35 40 45  
 Leu Thr Arg Gly Trp Gly Arg Ala Trp Pro Trp Lys Gln Ile Leu Lys  
 50 55 60  
 Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly Ala  
 65 70 75 80  
 Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg Ser  
 85 90 95  
 Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val Glu  
 100 105 110  
 Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu Phe  
 115 120 125  
 Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys Val  
 130 135 140  
 Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys Pro  
 145 150 155 160  
 Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu Asn  
 165 170 175  
 Ala Ser Ser Asn His Asp His Asp Asp Gly Ala Ser Gly Thr Pro Lys  
 180 185 190  
 Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala Lys  
 195 200 205  
 Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn Glu  
 210 215 220  
 Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile Gly  
 225 230 235 240  
 Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys Val  
 245 250 255  
 Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys Arg  
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